

GenCore version 5.1.9
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score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

OM protein - nucleic search, using frame_plus.p2n model

Run on: September 18, 2006, 00:41:40 ; Search time 4618 Seconds

(without alignments)
 7156.415 Million cell updates/sec

Title: US-10-733-816-2

Perfect score: 2081

Sequence: 1 MEYMPMEGGEMSGRPTTSF.....QELSSNPPLATLIPPHARI 394

Scoring table: BLOSUM62

Xgapop 10.0 Xgapext 0.5
 Ygapop 10.0 Ygapext 0.5
 Fgapop 6.0 Fgapext 7.0
 Delop 6.0 Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 9647396

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
 -MODEL=frame+ p2n.model -DEV=xip
 -Q=/abs/ABSSWEB/spool/US1033816/runat_15092006_084446_15519/app_query.fasta_1
 -DB=EST -QMT=fasap -MINLEN=0 -LOOPEXT=0
 -UNIT=S-bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=BLOSUM62 -LIST=45
 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -MIN=0 -ALIGN=15 -NODE=LOCAL
 -OUTFILE=pto -NORM=ext -HEAPSZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03p
 -USER=US1033816 @CGN 1.1.9228 @runat_15092006_085446_15519 -ICPU=6 -ICPU=3
 -NO_MMAPP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -KGAP0P=10 -KGAPEXT=0.5 -FGAP0P=6 -FGAPEXT=7
 -YGRPOP=10 -YGRPEXT=0.5 -DEL0P=6 -DELEXT=7

Database :

EST: *

1: qb_est1:*

2: qb_est3:*

3: qb_est4:*

4: qb_est5:*

5: qb_est6:*

6: qb_htc:*

7: qb_est2:*

8: qb_est7:*

9: qb_est8:*

10: qb_est1:*

11: qb_gss1:*

12: qb_gss1:*

13: qb_gss1:*

14: qb_gss1:*

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB ID	Description
1	2015	96.8	2312	6 AK170965	AK170965 Mus muscu
2	2015	96.8	2847	6 AK154293	AK154293 Mus muscu
3	2013	96.7	1732	6 CR617019	CR617019 full-leng
4	1609	77.3	1897	6 CR610570	CR610570 full-leng
5	1609	77.3	2119	6 CR615336	CR615336 full-leng
6	1609	77.3	2124	6 CR593340	CR593340 full-leng
7	1594	76.6	1760	6 CR597295	CR597295 full-leng
8	1594	76.6	3536	6 CR749620	CR749620 Homo sapi
9	1556	74.8	1094	10 W18183	W18183 IMAGE:20087
10	1446	69.5	841	9 CX75595	CX75595 JGI_CAAJ1
c 11	1415	68.0	818	9 DN530922	DN530922 135786 M
c 12	1410.5	67.8	993	8 CO579074	CO579074 ILMIGEN
c 13	1403	67.4	869	10 DT19300	DT19300 JGI_CAAK1
c 14	1387	66.7	2190	6 AK164048	AK164048 Mus muscu
c 15	1379	66.3	890	3 BG651422	BG651422 AGENCOURT
c 16	1368	65.7	844	10 DV123624	DV123624 LB13017.C
c 17	1362.5	65.5	931	1 AL536089	AL536089 AL536089
c 18	1336	64.2	946	1 AL521664	AL521664 AGENCOURT
c 19	1334.5	64.1	930	3 BG651351	BG651351 AGENCOURT
c 20	1333	64.1	935	4 CA976264	CA976264 AGENCOURT
c 21	1318.5	63.4	1094	2 BM478839	BM478839 JGI_CAAV9
c 22	1317	63.3	774	4 CB165245	CB165245 72614 MA
c 23	1316	63.2	812	8 CV557169	CV557169 UI-M-H2O-
c 24	1315	63.2	863	10 DT280981	DT280981 JGI_CAAV9
c 25	1312	63.0	749	4 CB654030	CB654030 705088 MA
c 26	1308	62.9	886	3 BG654247	BG654247 AGENCOURT
c 27	1295	62.3	747	2 BI558388	BI558388 60324049
c 28	1291	62.0	800	10 DT154092	DT154092 JGI_ANNO3
c 29	1268	60.9	889	3 BQ673346	BQ673346 AGENCOURT
c 30	1266	60.8	927	3 BO659839	BO659839 AGENCOURT
c 31	1263.5	60.7	1275	13 CL963186	CL963186 Os.FCC008
c 32	1259	60.5	1745	6 AY106255	AY106255 Zea mays
c 33	1257.5	60.4	1752	6 AY108486	AY108486 Zea mays
c 34	1256	60.4	785	5 CK468065	CK468065 93930 MA
c 35	1255	60.3	781	10 DV907419	DV907419 LB2282.CR
c 36	1253.5	60.2	1197	13 CI957492	CI957492 Os.FCC000
c 37	1247	59.9	1967	6 AY103545	AY103545 Zea mays
c 38	1245	59.8	785	5 CK465964	CK465964 937126 MA
c 39	1240.5	59.6	755	2 BG210727	BG210727 RST0273
c 40	1233	59.3	1666	6 AY104068	AY104068 Zea mays
c 41	1232	59.2	1409	6 CNS0BFT	B81815323 Arabidops
c 42	1232	59.2	1461	6 CNS0B1V	B81817800 Arabidops
c 43	1231	59.2	1711	6 DQ241848	DQ241848 Solanum t
c 44	1228	59.0	1593	6 DQ225208	DQ225208 Solanum t
c 45	1225	58.9	1638	6 CNS09YSF	BK8313446 Arabidops

ALIGNMENTS

RESULT 1 AK170965
 LOCUS AK170965 mRNA linear HTC 21-SEP-2005
 DEFINITION Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN

Pred. No. is the number of results predicted by chance to have a

- full-length enriched library, clone: F630213P21 product: glycogen synthase kinase 3 beta, full insert sequence.
- ACCESSION NUMBER** AK170965
VERSION AK170965.1
KEYWORDS HTC; CAP trapper.
ORGANISM *Mus musculus* (house mouse)
- REFERENCE 1**
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL *Meth. Enzymol.* 303, 19-44 (1999)
PUBMED 10349636
- REFERENCE 2**
AUTHORS Carninci, P., Shibata, Y., Hayayasu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL *Genome Res.* 10 (10), 1617-1630 (2000)
PUBMED 11042159
- REFERENCE 3**
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Muramatsu, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujimoto, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawai, J., Okazaki, Y., Muranotsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL *Genome Res.* 10 (11), 1757-1771 (2000)
PUBMED 11076681
- REFERENCE 4**
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okuzaki, Y., Gojobori, T., Itoh, M., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Mattioli, Y., Niwa, K., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Botello, D., Bojunga, N., Carninci, P., de Bonafo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Garibaldi, M., Gustincich, S., Hill, D., Holmann, M., Hume, D.A., Lyons, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Monbaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Rodriguez, I., Schonbach, C., Seye, A.T., Shibusawa, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Westz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
CONSORTIUM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
- TITLE** Functional annotation of a full-length mouse cDNA collection
JOURNAL *Nature* 409 (6821), 685-690 (2000)
PUBMED 11117751
- REFERENCE 5**
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Obata, N., Saito, R., Suzuki, H., Yamamoto, A., Kiyosawa, H., Yogi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Cousins, S., Dalla, S., Dragani, T.A., Chothia, C., Corbani, L.E., Frazer, K.S., Gaasterland, T., Fletcher, C.F., Forrest, A., Jarvis, E.D., Kana, A., Gariaboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Macchioni, L., McKenzie, L., Mikl, H., Nagashima, T., Numata, K., Okido, T., Pavani, W.J., Perez, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Secou, M., Shimada, K., Verardo, R., Takenaka, Y., Taylor, M.S., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamamoto, H., Zabavsky, E., Zhu, S., Zimmer, A.,

- | | | | | |
|------|--|------|------------|--|
| 181 | TyrosineSerineGlycylcysteineAsparagineProlineSerineAsparagineLeucineLeucineAsp | 200 | JOURNAL | High-efficiency full-length cDNA cloning |
| 1483 | TATATCCATTCTTGGATCTGCCATCAGATAAACACAGAACCTCTGTGAT | 1542 | METHOD | Mech. Enzymol. 303, 19-44 (1999) |
| b | | | REFERENCE | 10349636 |
| b | | | AUTHORS | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Ichii, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, K. |
| b | | | TITLE | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes |
| b | | | JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) |
| b | | | PUBLISHED | 11/04/2019 |
| b | | | REFERENCE | Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akizawa, J., Nishi, K., Kisanuki, T., Tashiro, H., Itoh, M., Saito, N., Ishii, Y., Nakamura, S., Haizawa, M., Niishine, H., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasihigaki, M., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Inukaiwa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. |
| b | | | AUTHORS | RIKEN integrated sequence analysis system - 384-format sequencing pipeline with 384 multicapillary sequencer |
| b | | | JOURNAL | Genome Res. 10 (11), 1757-1771 (2000) |
| b | | | PUBLISHED | 11/07/2001 |
| b | | | REFERENCE | Kawai, J., Shinagawa, A., Shiba, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Niimi, K., Kiyoysa, M., Yamana, I., Saito, T., Okazaki, Y., Goboroi, T., Bono, H., Konosawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gibbs, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Peacock, G., Quackenbush, J., Schriml, L.M., Staabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakamoto, N., Sasai, K., Okido, T., Furui, M., Aono, H., Baldwin, R., Barsh, G., Blake, J., Boffelli, D., Bojtan, C., N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Garibaldi, M., Gustincic, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, L., Mombaert, P., Nordone, F., Ring, B., Ringwald, M., Roederuez, I., Sakamoto, Y., Nogami, A., Schonbach, C., Goboroi, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Betzel, K.W., Blake, J.A., Bradic, P., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Goboroi, T., Baldarelli, R., Hill, D.P., Carninci, P., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsuki, S. and Hayashizaki, Y. |
| b | | | AUTHORS | RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium |
| b | | | TITLE | Functional annotation of a full-length mouse cDNA collection |
| b | | | JOURNAL | Nature 409 (6821), 685-690 (2001) |
| b | | | PUBLISHED | 11/21/2001 |
| b | | | REFERENCE | Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Niikaido, I., Osoato, N., Saito, R., Suzuki, H., Yamamoto, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Goboroi, T., Baldarelli, R., Hill, D.P., Carninci, P., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Betzel, K.W., Blake, J.A., Bradic, P., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gustincich, S., Gibbs, C., Godzik, A., Gough, J., Grimmond, S., Kiyosawa, H., Hirokawa, N., Jackson, J.I., Jarvis, B.D., Konai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kuroki, Y., Lee, I., Leonard, P., Margolin, M., Magot, D.R., Malatsky, L., Marchionni, L., McKenzie, L., Mikiti, H., Nagashima, T., Carninci, P. and Hayashizaki, Y. |
| b | | | ORGANISM | Mus musculus |
| b | | | DEFINITION | musculus NOD-derived CD1c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F630015J08 product: glycogen synthase kinase 3 beta, full insert sequence. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus (house mouse) |
| b | | | ORGANISM | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293_2 GI:74178475 |
| b | | | SEQUENCE | AK154293 |
| b | | | KEYWORD | HTC 21-SEP-2005 |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | musculus NOD-derived CD1c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F630015J08 product: glycogen synthase kinase 3 beta, full insert sequence. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus (house mouse) |
| b | | | DEFINITION | Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293_2 GI:74178475 |
| b | | | SEQUENCE | AK154293 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
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| b | | | ACCESSION | AK154293 |
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| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
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| b | | | KEYWORD | HTC; CAP trapper. |
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| b | | | KEYWORD | HTC; CAP trapper. |
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| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
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| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
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| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
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| b | | | ACCESSION | AK154293 |
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| b | | | SOURCE | Mus musculus |
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| b | | | ACCESSION | AK154293 |
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| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
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| b | | | KEYWORD | HTC; CAP trapper. |
| b | | | SOURCE | Mus musculus |
| b | | | DEFINITION | Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. |
| b | | | ACCESSION | AK154293 |
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| b | | | KEYWORD | HTC; CAP trapper. |
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| b | | | ACCESSION | AK154293 |
| b | | | SEQUENCE | AK154293_1 GI:74178475 |
| b | | | | |

SRYRMLFLGATDYSISIDWSAGCTAELLGGOPIPGSDGVOLVELEIKVLTGP TROIIRMMNPNTFQIKHPVTFKRPKPPAALCSSLLETPARLPLEA CAHSFDFDLRDPAVYLKLPGNDRDTPLAFNFTTQELSSNPATLIPPHARIQQASPPA	Alignment Score: 3-110-733-816-2 (1-394) x AK154293 (1-2847)	Length: 2847	Qy 1.47e-210	Db 2015.00	Matches: 386	Conservative: 0	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
7 Gluglygly	-----MetSerGlyArgProArgThrThrSerPhe 20		Qy 2015.00	Db 98.0%			Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
974 GAGGAAARGCTGATTCAAGAGACCATCATGTCGGGGACCGAGAACCTCCCTI 1033			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
21 AlAGluSerCyslysProValGlnGlnProSerAlaPheGlyserMetLysValSerArg 40			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1034 GCGGAGAGCTGCAAGCCGTGCAAGCTTGTTGTTAGCATGAAAGTAGCAGA 1093			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
41 AbLyAspGlyserLyValThrValAlaThrProGlyLgypToSparg 60			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1094 GATAANGATGCCGCAAGGTAAACCAACAGTAGCTGGCAACTCTGGCTCTGACAGG 1153			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
61 ProGlnGluValSertThrAspThrlysValleLeiGlyAsnGlySerPheGlyValVal 80			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1154 CACAGGAAGTCACTATAAACAGAACATGAAATGATCATTTGGGTGCTSTA 1213			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
81 TyrGlnAlaLysLeuCysAspSerCysLeuValAlaLeiLysysValleUgluAsp 100			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1214 TATCAAGCCAAACTTGTGATCTCGAGACTGTGTCATCACAGAAAGTCTACAGGAC 1273			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
101 LysArgGlyLysAsnArgGluLeuGlnIleMetArgLysLeuAspLysCysAsnIleVal 120			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1274 AACGGATTAGAACCGAGCTCCAATGCTGAGAAAGCTAACACTGTRACITGC 1333			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
121 ArgLeuArgTyrrPheHeterSerSerGlyGluLysAspGluValAlaLys 140			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1334 CGACTGGTATCTCTACTCGACTGCGGAGAAAGATACTGTTAACCTTAACCT 1393			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
141 ValLeuAspPheValProGlyLysValtyArgValAlaLysTySerArgGlyLys 160			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1394 GTCTGGACTATGTTCCGGAGAACCTGACAGTGAGCTGCGGAGAACACTATAGTCGAGCAG 1453			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
161 GluThrLeuProValIleTyryValLysLeuUtrMetTyrglyLeuLeuArgSerLeuAla 180			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1454 CAGACATCCCTGGATTAACCTGACTGTTGATGATCTGAGCTGAGAGTCGCC 1513			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
181 TyrLeuHisSerPheGlyIleCysHiSArgAspPileLysProGlnAsnLeuLeuAsp 200			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1514 TATATCCATTCTCTTGGATCTGCCATCCGACATTAACCAAGAACCTCTTGTGAT 1573			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
201 ProaspThrAlaValleLysLeucysAspPheGlySerAlaLysGlnLeuValArgLys 220			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1574 CTCGATACAGCTGTTAAACTGCTGACTGTTGATGATCTGAGCTGAGCTGCC 1633			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
221 GluProAsnValSerTyrLysSerArgTyrrPheValGlyLeuLeuPhePheLys 240			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:
1634 GAGCCCAATGTTCTATATCTGTCGACTGACTGAGCTGAGCTGATCTGTTGAG 1693			Qy 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 98.0%	Db 96.8%	Db 6	Db 3:

into the Not I and Ecor V sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1. .1732
`/organism="Homo sapiens"`
`/mol_type="mRNA"`
`/db_xref="s606"`
`/clone="CSUDB031J02"`
`/tissue_type="Neuroblastoma Cot 10-normalized"`
`/nucleotide="nCMVSPORT 6"`

Qy	90	GluLeuValAlaIleTyrLysValLeuGlnAspLysArgPhenylAlaAsnArgGluLeuGln	109	
Parady Avenue 2 (bases 1 to 1897)	Qy			
AUTHORS Genoscope.	Db	587	GAACATGTCGCCCTCAGAGGTCTCCAGAACAGGTCAAGACGAGCTGCAG	
JOURNAL Direct Submission	Qy	587	546	
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 131, 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Web : www.Genoscope.cns.fr)	Db	647	IleMetArgLysLeuAsnAspHisCysAsnIleValLeuGlnAspTyrPheHpyThrSerSer 129 ATCATCGTAAGCTGACCATCTGAAATTCATTTCTACTCCAGT	
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	Qy	130	GlyGluLeuLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrVal 149 : : : : : : : : : : : 707 GCGGAAGAAGAACGAGCTTACCTAAATCTGGCTGGAAATGATCTGCCGAGACATG 765	
Location/Qualifiers 1..1897	Qy	150	TyrArgValAlaArgHistYsTyrSerArgGlyAlaGlnLeuProValLeuTyrValLeu 169 : : : : : : : : : : 767 TACCGGGGCGCCGCACTACCAAGCGTACATCCATCCTATGAGTACCAATCCTGACAG 826	
source /organism "Homo sapiens" /mol_type "mRNA" /db_xref "Taxon:9606" /clone "CSBDJ012Y04" /tissue _type "T cells (Jurkat cell line) Cot 10-normalized" /plasmid "pCMVSPORT_6"	Qy	170	LeuTyrMetTyrClnLeuPheArgSerLeuIleTyrIleHisSerPheGlyIleCysHis 189 : : : : : : : : : 827 GNGTACATCTACAGCTTCGGCACTGCTGCTGCCCCAAATGCTCTCACATCGTCT 886	
SATURATES	Db	887	ArgAspBilelysProGlnAsnLeuLeuAspProAspPheAlaValLeuLeuLeuAsp 209 : : : : : : : : Db	887 CGGACATCAAGCCCAGAACCTCTGTGACACTCTCCAGCTCTCTCCAGCTGC 946
TRIGGIN	Qy	210	AspPheGlySerAlaGlnLeuValArgGlyGluProAsnValSerTyrIleCysSer 229 : : : : : : : 947 GATTTCGGAGTCGAAAGCAAGCTGGTCCGAGGGGCCAAATGCTCTCACATCGTCT 1006	
Significance Scores:	Db	947	ArgTyrTyrArgAlaProGluLeuIleIleGlyAlaIleAspTyrThrSerSerIleAsp 249 : : : : : : Db	1007 CGTACTACGGGCCAGAGCTCTTGGGACTGATACTTGGGACTGATCATCCATGAT 1065
Protein ID: CR610570 (1..1897)	Qy	250	ValTrpSerAlaGlyCysValLeuAlaGluLeuLeuIleGlnProIlePheProGly 269 : : : : : Db	1067 GTTGTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1126
Length: 1897	Qy	270	AspSerGlyValAspGinLeuValGluIleIleIleValGluIleIleIleValGluIle 269 : : : : Db	1127 GCAAGTGGGGACGGACGCTGTTGGAGATCATAGGGCTCTGGAGATCATAGGG 1166
Matches: 319	Qy	310	ProTrpIleIleValPheArgProArgThrProProGluIleIleLeuIleLeuIle 329 : : : : Db	1247 CCCTGGACAGGGTGTCAATTCGAGGGCCCTTCGGCTCTGTCTGCTG 1306
Conservative: 24	Qy	310	GlnIleArgGluIleAsnProAspTyrThrGluIleIleLeuIleLeuIleLeuIle 305 : : : : Db	1187 CAAATCCGAGATGAACTACAGCGGTTCAACTCCCTCAGATTAAGCTCAC 1246
Mismatches: 43	Qy	330	LeuIleArgLeuIleAsnProAspTyrThrGluIleIleLeuIleLeuIleLeuIle 369 : : : : Db	330 LeuLeuGluIleIleThrProThrAlaArgLeuIleProLeuIleAlaHisSerPhe 349
Indels: 58	Qy	330	1307 CTCCTGGAGTAGACCCCATCTCAAGGCTCTCCAGTCAACTCCCTCTGCGCAAGCTCT 13:6	
Gaps: 4	Db	350	PhAspAspDipeptideAspProAsnValAlaIleGlyArgAspThrProAlaLeu 369 : : : Db	1367 TTGTGAACTGGCATGTCGAGACCCAGCTGGACCCACTTCACCTCCCTCTC 1426
-----	Qy	370	PheAsnPheThrThrGlnGluLeuUserSerAsnProProLeuIleThrIleLeuIle 389 : : Db	1427 TTCAACTCTGCTGCTCATCCACCGTCTCTCATCCACGGCATCTTATCCCT 14:6
-----	Qy	390	ProHisAlaArg 393	

	JOURNAL	REMARK
Qy	Unpublished	Contact : Feng Liang Email : fliang@lifetech.com URL : http://Fulleng.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1760)
Db	REFERENCE	Genoscope.
Qy	AUTHORS	Direct Submission
Db	TITLE	Genoscope - Centre National de Séquençage :
Qy	JOURNAL	Submitted (20-JUL-2004) Genoscope - FRANCE (E-mail : seqref@genoscope.cns.fr)
Db	COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Qy	FEATURES	Location/Qualifiers
Db	source	1. .1760 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DF022YM11" /tissue_type="Fetal brain" /plasmid="pCMVSPORT_6"
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Db	Alignment Scores:	
Qy	Pred. No.:	2.24e-164
Db	Score:	1594.00
Qy	Percent Similarity:	92.0%
Db	Best Local Similarity:	85.8%
Qy	Query Match:	76.6%
Db	DB:	6
Qy	Length:	1760
Db	Matches:	301
Qy	Conservative:	22
Db	Mismatches:	28
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Db	Gaps:	0
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Db	Db	1189 CCGTGACAAAGGTCTCAATCTGAGCCATCCGGCAAGGCCATCGCTCTAGC 1248
Qy	Qy	330 LeuLeuGluLysThrProLeuGluAlaCysAlaHisSerPhe 349
Db	Db	1249 CTGCTGGAGAACCCCCATCTCAAGGTCTCCCACAGGCTCTGGCACAGCTC 1308
Qy	Qy	350 PheAspGluLeuArgAspProAsnValByshisProAspThrProAlaLeu 369
Db	Db	1309 TTGTATGACTGCATGTCTGGACCACTTCCTCTTC 1368
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Db	Db	1369 TTCAACTTCAGCTGGAATCTCCACGCCATCTCAACCCCATCTTATCCT 1428
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Qy	RESULT 7	
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DEFINITION	full-length cDNA clone CS0DF022YM11 of Fetal brain of Homo sapiens (human).	
ACCESSION	CR597295	
VERSION	GI:50478102	
KEYWORDS	HTC; CNSLT_CDNA.	
SOURCE	Homo sapiens (human)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1 (bases 1 to 1760)	
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.	
TITLE	Full-length cDNA libraries and normalization	
Qy	103 PheAspAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAlaIleValArgLeu 122	
Db	Qy	183 TCCAGBACGACCGAGGCTGCGAGATCGGTAAAGCTGACACTGCAATAATTGAGGCTG 242
Qy	123 ArgTrpPhePhiThrSerSerGlyGluLysBlysAspGluIvalIysValLeuAlaLeu 142	
Db	Qy	243 AGATACTTTCTACTCCAGGGAGAAGAGGAGCTTACCTAACTCGGTGAGGCTG 302
Qy	143 AspTyrValProGluThrValValArgIleArgIleArgAlaLysGlnThr 162	
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Db	86	GTACCCACTCTAGCCGCGCCGCGGTGAAGCTGGCCGAGGAGTCACAGTC	145	Db	986	GARGACTGGATGTCGGMAACCCAGCTGCATACACGCCACATCTCCCTCTTC	1045
Qy	71	ValIleGlyAsnGlySerPhesIvaValtrygInalaLysLeucyAspSerGlyGlu	90	Qy	371	AsnPheThrThrGlnGluLeuSerSerAsnProProLeu	:383
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	REFERENCE						
	1	(bases 1 to 841)					
	AUTHORS						
	Richardson,P., Lucas,S., Pokornar,D., Detter,J.C., Ng,D.C.,						
	Brokstein,P. and Lindquist,E.A.						
	TITLE						
	DOE Joint Genome Institute Xenopus tropicalis EST project						
	JOURNAL						
	Unpublished (2004)						
	COMMENT						
	Other ESTs: JGI_CRAJ11693.rev						
	CONTACT						
	Lindquist,E.A., Richardson,P.						
	DOI						
	Joint Genome Institute						
	http://www.jgi.doe.gov						
	DNA						
	Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov						
	Clone						
	Distribution: Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley: http://tropicals.berkeley.edu/home)						
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	FEATURES						
	source						

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Score:	1410.50	Matches:	274	Db	785	ACAAAGCTGTCAAAATCTGAGCCATTCGGCTCGCTAACCTGCTG	844						
Percent Similarity:	88.6%	Conservative:	22	Qy	332	GluGlyThrProThrAlaArgLeuThrProLeuGluCysAlaHisSerPhe-Phe	351	Db	845	GATGACCCCGCCCTAACAGCTCCGGCTAACAGCTCCGGCTAACAGCTCCGG	904		
Best Local Similarity:	80.0%	Mismatches:	25	c				Db	905	AGAACTGCGAARGCCGGG-----AACCCCAGTCCCCCTTA	957		
Query Match:	67.8%	Indels:	13					Db	905	AGAACTGCGAARGCCGGG-----AACCCCAGTCCCCCTTA	957		
DB:	8	Gaps:	2					Qy	351	sgGluleuArgAspProAsnVallysProAsnGlyArgAspThrProAlaLeuPhe	371		
US-10-733-816-2 (1-394) x C0579074 (1-993)													
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Vertebrata;				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
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AUTHORS				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
Richardson,P., Lucas,S., Rokhsar,D., Dettner,J.C., Ng,D.C.,				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
Brookstein,P. and Lindquist,E.A.				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
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Lindquist,E.A., Richardson,P.				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
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280 Mitchell Drive, Walnut Creek, CA 94598, USA				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
Tel: 925 296 5600				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
Fax: 925 296 5710				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
Email: canajgi-psf.org				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
CDNA Library Preparation: DOE Joint Genome Institute:				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
http://www.jgi.doe.gov				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
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the JGI Clone ID and the direction of sequencing. The suffix ".fwd"				Db	958	-----CCCCCCCCCTT-----CCCCCCCCCTT	969						
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- Aarakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,M., Izawa,M., Nishi,K., Kiyosawa,H., Matsuda,S., Yamamoto,I., Saito,T., Oizaki,Y., Gojori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batzalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gibbs,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,B., Tomita,M., Wagner,L., Washio,T., Yuki,T., Furuno,M., Ano,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bottinga,N., Carninci,P., de Bonald,M.P., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Garibaldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J.J., Mazzarilli,J., Monbaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakai,K., Okido,T., Sato,K., Schonbach,C., Seya,T., Shibusawa,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Wetzel,C., Whitaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsukii,S., and Hayashizaki,Y.
- RIKEN Genome Exploration Research Group Phase II Team and the RANTOM Consortium
- FUNCTIONAL annotation of a full-length mouse cDNA collection**
- TITLE** Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6621), 685-690 (2001)
PUBMED 11217851
5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nakaido,I., Osato,N., Saito,R., Tomaru,Y., Yamamoto,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blaize,J.A., Bradt,D., Brusic,V., Chotila,C., Corbani,L.E., Cousins,S., Dalla,S., Dregan,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Garibaldi,M., Gassi,C., Gozik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanaai,A., Kawaji,H., Kawai,Y., Kezierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y.Y., Lehardt,B., Lyons,P.A., Maglott,D.R., Maltsev,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavani,W.J., Perera,G., Petrosky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Seton,M., Shimoda,K., Sultan,R., Takemoto,Y., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynnshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Sato,K., Shiraki,T., Kawai,K., Aizawa,K., Sakaizumi,N., Sato,K., Shiraki,T., Kawai,J., Aizawa,K., Itoh,M., Kagawa,T., Hara,A., Hashizume,W., Inotani,K., Ishii,Y., Shinagawa,A., Yasunishi,A., Yoshiro,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E., and Hayashizaki,Y.
- CONSRIM**
- TITLE** Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466651
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AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Rogers,J., Birney,E., and Hayashizaki,Y.
- CONSRIM**
- TITLE** The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
7
AUTHORS Nakayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Suzuki,M., Kawai,J., Suzuki,M., Kawai,J., Suzuki,H., Nakamura,M., Nishida,H., Sap,C.C., Suzuki,M., Kawai,J., Suzuki,M., Nishida,H., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Inamuro,K., Ichih,M., Kato,T., Kawaji,H., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Niromiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Watanuki,A., Okamura-Ohno,Y., Suzuki,H., Kawai,J., and Hayashizaki,Y.
- CONSRIM**
- TITLE** The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE Nakayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Suzuki,M., Kawai,J., Suzuki,M., Kawai,J., Suzuki,H., Nakamura,M., Nishida,H., Sap,C.C., Suzuki,M., Kawai,J., Suzuki,M., Nishida,H., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Inamuro,K., Ichih,M., Kato,T., Kawaji,H., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Niromiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Watanuki,A., Okamura-Ohno,Y., Suzuki,H., Kawai,J., and Hayashizaki,Y.
- RIKEN Genome Exploration Research Group**
- TITLE** Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
8
AUTHORS Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Martick,J., Hume,D.A., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghiri,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B., and Wahlestedt,C.
- RIKEN Genome Exploration Research Group**
- TITLE** Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashizaki,K., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Niromiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazumi,N., Sano,H., Saeki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watanuki,A., Muramatsu,M., and Hayashizaki,Y.
- RIKEN**
- TITLE** Direct Submission
JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

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 Fax: +81-45-503-9216

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed preprint mouse tissues.

Please visit our web site for further details.
<http://genome.gsc.riken.jp/>

Location/Qualifiers

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Attribute

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- GB|BC0006936, evidence: BLASTN, 100%, match=788) putative"

• FEATURES

• Location/Qualifiers